

What is claimed is:

1. A method for detecting the presence or absence or amount of an experimental target-specific probe on a substrate comprising:

exposing a substrate containing a first feature comprising an experimental target-specific probe and a control-specific probe to a labeled control target, such that the labeled control target binds specifically to control-specific probe bound to the substrate, and

measuring a signal from labeled control target bound to control-specific probe to determine the presence or absence or amount of experimental probe.

2. The method of claim 1, wherein the experimental target-specific probe and control-specific probe are polynucleotides.
3. The method of claim 2, wherein the control-specific probes that are polynucleotides contain synthetic non-Watson-Crick bases.
4. The method of claim 1, wherein the control-specific probe is attached to the experimental target-specific probe.
5. The method of claim 1, wherein the control-specific probe is not attached to the experimental target-specific probe.
6. The method of claim 1, wherein the labeled control target comprises a fluorophore.

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7. The method of claim 1, wherein the substrate is exposed to a labeled experimental target molecule in a sample, such that labeled experimental target molecule is bound to experimental target-specific probe.
8. The method of claim 7, wherein the signal from labeled control target bound to control-specific probe is used to quantitate the amount of labeled experimental target molecule in a sample.
9. The method of claim 1, wherein the substrate further contains a second feature comprising a second experimental target-specific probe and the control specific probe.
10. A method for detecting the presence or absence or amount of an experimental target probe on a substrate comprising:
- exposing a substrate containing a feature comprising an experimental target probe to a labeled control target, such that the labeled control target binds to experimental target probe bound to the substrate, and
- measuring a signal from labeled control target bound to experimental target probe to determine the presence or absence or amount of experimental probe.
11. A kit comprising:
- a substrate comprising a feature containing an attached experimental target-specific probe and an attached control-specific probe, and

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a labeled control target, wherein the labeled control target binds specifically to the control-specific probe, and does not bind specifically to the experimental target-specific probe.

12. The kit of claim 11, wherein the control-specific probe, experimental target-specific probe, and the labeled control target are polynucleotides.
13. The kit of claim 12, wherein at least the control-specific probe and the labeled control target contain non-Watson-Crick base pairs.
14. The kit of claim 11, wherein the control-specific probe is attached to the experimental target-specific probe.
15. The kit of claim 11, wherein the control-specific probe is not attached to the experimental target-specific probe.
16. A synthetic control for use in a nucleic acid array, comprising a pool of different control polynucleotides attached to labels, wherein each control polynucleotide is designed to complement a polynucleotide that is attached to a feature in the array.
17. The synthetic control of claim 16, wherein the different control polynucleotides complement different expressed transcripts or alleles of a specific species of organism.
18. The synthetic control of claim 17, wherein the species is selected from a human, rabbit, mouse, and rat.
19. The synthetic control of claim 16, wherein the different control polynucleotides complement a broad range of expressed transcripts of a specific sample type.

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20. The synthetic control of claim 19, wherein the sample type is selected from whole blood, peripheral blood lymphocytes, hair, semen, lymph, amniotic fluid, cerebrospinal fluid, placental tissue, vaginal tissue, sputum, and skin.
21. The synthetic control of claim 16, wherein the different control polynucleotides are short sequences comprising random nucleotides.
22. The synthetic control of claim 21, wherein the different control polynucleotides are designed such that the pool of different control polynucleotides will complement any probe attached to a nucleic acid array.
23. The synthetic control of claim 22, wherein the different control polynucleotides comprise bases or linkages that are chemically modified such that the different control polynucleotides have a TM above that of naturally occurring nucleotides.
24. The synthetic control of claim 23, wherein the bases are linked by peptide bonds.
25. The synthetic control of claim 21, wherein the different control polynucleotides are 9 or 10 bases in length.
26. A method for determining the relative amount of two different experimental target nucleic acid sequences in a sample, comprising:

providing a nucleic acid array, wherein the array comprises a first feature that comprises first experimental target-specific probes that are complementary to a first experimental target sequence and control-specific probes that do not hybridize to experimental target sequences, and a second

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feature that comprises second experimental target-specific probes that are complementary to a second experimental target sequence and control-specific probes that do not hybridize to experimental target sequences;

contacting the array with:

- (1) a sample that includes experimental target sequences that are labeled with a first label; and
- (2) synthetic control target sequences that are labeled with a second label and that hybridize to the control-specific probes on each of the first and second features, but that do not hybridize with the experimental target-specific probes;

determining the intensity of any signal from the first and second labels in the first and second features;

determining the ratio of the intensity of the signal from the first label to the intensity of the signal from the second label for each of the first and second features; and

comparing the ratios of the intensity of the signal for the first and second features to calculate the relative amount of first and second experimental nucleic acid target sequences in the sample.

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